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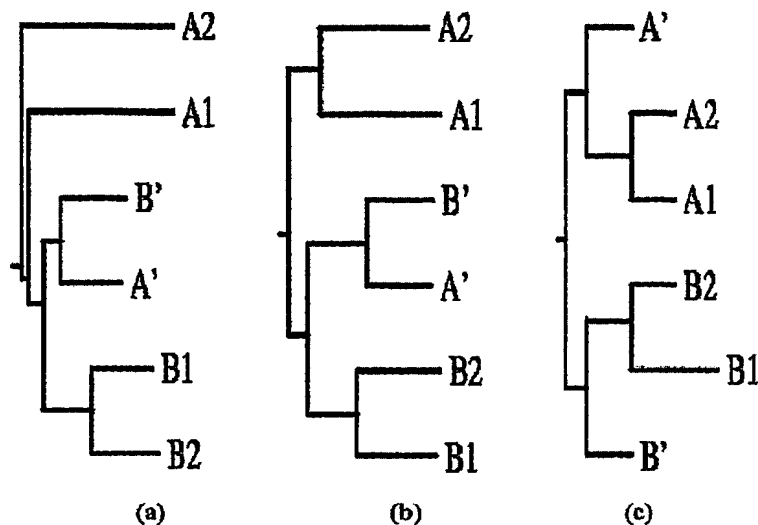
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(54) Title: SYSTEM AND METHOD FOR SEQUENCE DISTANCE MEASURE FOR PHYLOGENETIC TREE CONSTRUCTION



(57) Abstract: The present invention permits identification of biological materials following recovery of DNA using standard techniques by comparing a mathematical characterization of the unknown sequence with the mathematical characterization of DNA sequences of known genera and species. The clinical identification of infectious organisms is required for accurate diagnosis and selection of antimicrobial therapeutics. The invention allows an *ab initio* approach with the potential for rapid identification of biological materials of unknown origin. The approach provides for identification and classification of emergent or new organisms without previous phenotypic identification. The technique may also be used in monitoring situations where the need exists for classification of material into broad categories of bacteria which could have an immediate impact on bio-terrorism prevention.



SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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